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GenCore version 5.1.4\_p5\_4578

OM nucleic - nucleic search, using sw model  
Run on: March 26, 2003, 11:15:29 ; Search time 12235 Seconds  
(without alignments)  
30.445 Million cell updates/sec

Title: US-10-086-184-1  
Perfect score: 23  
Sequence: 1 aaatcggtccggaggggaaac 23  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1615406 seqs, 8097743376 residues  
Minimum DB seq length: 0  
Maximum DB seq length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estapl: \*  
7: em\_estro: \*  
8: em\_hcc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_ntc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gbb: \*  
18: em\_gbb\_hum: \*  
19: em\_gbb\_inv: \*  
20: em\_gbb\_pth: \*  
21: em\_gbb\_vrt: \*  
22: em\_gbb\_fun: \*  
23: em\_gbb\_main: \*  
24: em\_gbb\_mus: \*  
25: em\_gbb\_other: \*  
26: em\_gbb\_pro: \*  
27: em\_gbb\_rnd: \*

RESULT 1  
AW248192  
DEFINITION AW248192 mRNA NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819671 5', mRNA sequence.  
ACCESSION AW248192  
VERSION AW248192.1  
KEYWORDS EST.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESPs: 2819671\_3prime  
Other: 2819671\_3prime  
Contact: Robert Stransberg, Ph.D.  
Email: cgrabs@MAIL.nih.gov  
Tissue Procurement: DCTP/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINC) DNA Sequencing by: Berkeley MCC sequencing  
project. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINC at: www.bio1nl.gov/bbri/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP Suite: POLY-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  
Contact: Robert Stransberg, Ph.D.  
Email: cgrabs@MAIL.nih.gov  
Tissue Procurement: DCTP/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINC) DNA Sequencing by: Berkeley MCC sequencing  
project. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINC at: www.bio1nl.gov/bbri/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP Suite: POLY-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center:

## ALIGNMENTS

c 7 12.2 53.0 40 9 AA939192 AA939192 092209.8  
c 8 11.8 51.3 37 9 AA174098 AA174098 tm05C07.X  
c 9 11.1 51.3 37 9 AA1740589 AA1740589 1M0215P10  
c 10 11.6 50.4 38 17 TA17C04Q AA166262 T. brucei  
c 11 11.6 50.4 39 17 A2800550 AA2800550 2M058B10  
c 12 11.4 49.6 36 9 AA825458 AA825458 oe64F12.B  
c 13 11.4 49.6 37 14 H43693 H43693 yob80b5.s1  
c 14 11.2 48.7 27 9 AU254533 AU254533 AU254523  
c 15 11.2 48.7 27 14 D18732 D18732 MUSGS1794  
c 16 11.2 48.7 31 9 AA920664 AA920664 VY4803.r  
c 17 11.2 48.7 37 13 B1561770 B1561770 60325684  
c 18 11.2 48.7 38 13 B1561718 B1561718 60325891  
c 19 10.8 47.0 22 9 AA985475 AA985475 0926089.B  
c 20 10.8 47.0 29 14 H55186 H55186 CHR20125.C  
c 21 10.8 47.0 32 17 A2813220 A2813220 2M0053P23  
c 22 10.8 47.0 33 17 A2803201 A2803201 2M0053A02  
c 23 10.8 47.0 34 9 AA517484 AA517484 vht79f07.r  
c 24 10.8 47.0 35 9 HSM0094 HSM0094 Homo sapii  
c 25 10.8 47.0 35 17 AZ469734 AZ469734 1M0283J19  
c 26 10.8 47.0 35 17 A2599526 A2599526 1M0414L22  
c 27 10.8 47.0 36 12 BF533462 BF533462 602069470  
c 28 10.8 47.0 37 9 A119467 A119467 983295.B  
c 29 10.8 47.0 37 9 A173501 A173501 ac10508.B  
c 30 10.8 47.0 37 17 TA168111P TA168111P A1734945 T. brucei  
c 31 10.6 46.1 34 10 BB385585 BB385585 601273926  
c 32 10.6 46.1 35 13 B1827700 B1827700 030374121  
c 33 10.6 46.1 37 9 A1538439 A1538439 tdd06C05.X  
c 34 10.6 46.1 38 12 BF687876 BF687876 60206947  
c 35 10.6 46.1 39 17 BH86648 BH86648 SALK\_1013  
c 36 10.6 46.1 40 9 A1697005 A1697005 wc769G7.X  
c 37 10.4 45.2 26 17 BH759478 BH759478 KG0415-5  
c 38 10.4 45.2 34 9 AA389345 AA389345 am64d06.B  
c 39 10.4 45.2 34 10 AV833436 AV833436 AV833436  
c 40 10.4 45.2 37 10 AV95431 AV95431 AV95431  
c 41 10.4 45.2 37 17 TA21B11P TA21B11P AV478555 T. brucei  
c 42 10.4 45.2 40 9 A1424339 A1424339 te95el1.X  
c 43 10.4 45.2 40 17 BH857109 BH857109 SALK\_0768  
c 44 10.2 44.3 29 10 AW250348 AW250348 282197.5  
c 45 10.2 44.3 32 12 BG718358 BG718358 60269367

http://www.genome.washington.edu Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 39 contiguous distinct Peaks following vector sequence.

Plate: LIGM2 row: D column: 8. Location/Qualifiers

FEATURES source

1. .39 /organism="Homo sapiens" /db\_xref="Taxon:9606" /clone="IMAGE:2019671"

BASE COUNT

7 a 11 c 17 g 4 t

ORIGIN

Query Match 54.8%; Score 12.6; DB 10; Length 39; Best Local Similarity 78.9%; Pred. No. 1.5e+05; Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAATGGCTCCGAGCGG 19

Db 14 AAGGCGGGCTGAGGCGG 32

RESULT 2

LOCUS AA938266 25 bp mRNA linear EST 27-AUG-1998 DEFINITION o097601.s1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1574136 3', similar to SW:Ch12\_MOUSE\_P28481 PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR ; mRNA sequence.

ACCESSION AA938266

VERSION AA938266.1

KEYWORDS GI:31096377

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (base 1 to 25) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

TITLE Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgaps\_r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Bennett-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/bbrp/image/image.html

Insert Length: 283 Std Error: 0.00

Seq primer: -40m13 fwd, 3' from Amersham

Trace considered overall poor quality

High quality sequence stop: 1.

Location/Qualifiers

FEATURES source

1. .34 /organism="Homo sapiens" /db\_xref="Taxon:9606" /clone="IMAGE:1951847"

/clone lib="Sores\_fetal\_lung\_NbHL19W" /dev\_stages="19 weeks" /lab\_host="DHL10B (ampicillin resistant)" /note="Organ: lung; Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'-TCTTACCAATGGAATGGGGGGCGCAATTGTTTGTGTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a C<sub>ot</sub> = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares

FEATURES source

1. .25 /organism="Homo sapiens" /db\_xref="Taxon:9606" /clone="IMAGE:1574136" /clone\_lib="NCI\_CGAP\_Kids5"

BASE COUNT

8 a 7 c 15 g 4 t

ORIGIN

Query Match 53.9%; Score 12.4; DB 9; Length 34;

/tissue\_type="2 pooled tumors (clear cell type)" /lab\_host="DHL10B" /note="Organ: kidney; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-AATCGAAAGATTCCGGGCCATATTGTTTGTGTTT-3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

RESULT 3

LOCUS AA1354718 34 bp mRNA linear EST 04-JAN-1999 DEFINITION IMAGE:1951847 3', similar to SW:PRPB\_HUMAN P02814 PROLINE-RICH PEPTIDE P-B; contains element MSRI repetitive element ; mRNA sequence.

ACCESSION A1354718

VERSION A1354718.1

KEYWORDS GI:4094871

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 34) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

TITLE Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

FEATURES source

1. .34 /organism="Homo sapiens" /db\_xref="Taxon:9606" /clone="IMAGE:1951847"

/clone lib="Sores\_fetal\_lung\_NbHL19W" /dev\_stages="19 weeks" /lab\_host="DHL10B (ampicillin resistant)" /note="Organ: lung; Vector: pRT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'-TCTTACCAATGGAATGGGGGGCGCAATTGTTTGTGTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a C<sub>ot</sub> = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares

Qy	1	AAATGGCTCCGAGGGAAA	22	EST.
Db	1		22	soybean.
REFERENCE				soybean.
AUTHORS				soybean max.
ORGANISM				Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Phaseoleae; Glycine.
1 (bases 1 to 37)				
Shoemaker, R., Klein, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Boila, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Schurk, R., Waterston, R. and Wilson, R.				
1 (bases 1 to 28)				
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				Public Soybean EST Project
Tumor Gene Index				Unpublished (1999)
Unpublished (1997)				Contact: Shoemaker R/Public Soybean EST Project
1 (bases 1 to 28)				Washington University School of Medicine
Trace considered overall poor quality				4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Possible reversed clone: similarity on wrong strand				Tel: 314 286 1800
High quality sequence stop: 1.				Fax: 314 286 1810
Location/Qualifiers				Email: est@watson.wustl.edu
1. 28				Trace considered overall poor quality
/organism="Mus musculus"				Available through: Rescan, Invitrogen Corp, 2130 South Memorial
/db_xref="taxon:10090"				Parkway Huntsville, AL 35801 For further information call: (800) 1-533-3163 or contact via email: ccr@resgen.com
/clone="IMAGE:1382557"				Seq prim: -40R from Gibco
/clone lib="Gm-c1013"				High quality sequence stop: 1.
/tissue_type="mammary gland"				Location/Qualifiers
/lab_host="DH10B"				1. .37
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified				/organism="Glycine max"
poli-linker; 1st strand cDNA was prepared from mammary				/db_xref="taxon:347"
gland tissue from a lactating female, and was then primed				/clone="GENOME SYSTEMS CLONE ID: Gm-c1013-1760"
with a Not I - oligo(dT) primer. Double-stranded cDNA was				/clone lib="Gm-c1013"
ligated to Eco RI adaptors (Pharmacia), digested with Not				/tissue_type="whole seedlings, 2-3 week old seedlings"
I and cloned into the Not I and Eco RI sites of the				/lab_host="XLI0-Gold"
modified pT7T3 vector. Library is normalized. Library				/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
was constructed by Bento Soares and M. Fatima Bonaldo."				XhoI; This cDNA library was constructed from mRNA isolated
BASE COUNT	10 a	9 c	8 g	from whole seedlings of 2-3 week old greenhouse grown
ORIGIN	7 a	18 C	2 g	plants. The cDNA library was prepared using the Stratagene
Query Match	53.0%	Score 12.2;	DB 9;	pBluescript II XR cDNA library construction kit
Best Local Similarity	82.4%	Pred. No. 2.1e+05;	Length 28;	Complementary DNA was synthesized from mRNA using a primer
Matches	14;	Conservative 0;	Mismatches 3;	consisting of a poly (dT) sequence with a XhoI restriction
Qy	6	GGCTCGAGGGGGAAA	22	site. EcoRI adapters were ligated to the blunt-ended cDNA
Db	5	GGCCCCAGGGGGAAA	21	fragments followed by XhoI digestion. The cDNA fragments
RESULT 5				were directionally cloned into the EcoRI-XhoI restriction
A196055/C				site of the pBluescript vector. The ligated cDNA fragments
A196055				were transformed into XLI0-Gold host cells. This library
SC6d04_Y1				was constructed by Dr. Randy Shoemaker and Dr. John
Gm-c1013-1760				Erpelding."
REACTION CENTRE SUBUNIT II PRECURSOR				
ACCESSION	A196055			
VERSION	A196055.1			
KEYWORDS				
TA381B01Q/c				
TA381B01Q				
DEFINITION				
T. brucei sheared genomic DNA clone 381b01, reverse sequence,				
genomic survey sequence.				
ACCESSION	AL497653			
VERSION	AL497653.1			
KEYWORDS				
GSS.				



Average insert size 1.7 kb. Life Technologies catalog #:

BASE COUNT 6 a 11531-019\*  
9 c 21 g 1 t

ORIGIN Query Match Best Local Similarity 51.3%; Score 11.8; DB 9; Length 37; Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAATGGCTCGAGGGGAAAC 23  
Db 1 AAAGGGGCCCCGGGGCCAC 23

RESULT 9  
A2430589  
DEFINITION A2430589 39 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0215F10 Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0215F10 P, DNA sequence.  
ACCESSION A2430589  
VERSION A2430589.1 GI:10554602  
KEYWORDS GSS.  
SOURCE hohe mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 39)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid insert  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0215 Row: P Column: 10  
Seq primer: CCTGTGAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 39.

FEATURES  
source  
1. .39  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGIM0215F10"  
/clone\_1bb="Mouse 10kb plasmid UGCGIM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
/note="Vector: PWD4Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource/documents/dnares/". The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|47321149b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into

BASE COUNT 1 a 17 c 15 g 6 t  
ORIGIN Query Match Best Local Similarity 51.3%; Score 11.8; DB 17; Length 39; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGGCTCGAGGGGG 19  
Db 13 CGCTTCCACGGG 27

RESULT 10  
TA137C040  
DEFINITION TA137C040 38 bp DNA clone 137c04, reverse sequence, T. brucei. sheared genomic DNA clone 137c04, reverse sequence, genomic survey sequence.  
ACCESSION AL466262  
VERSION AL466262.1 GI:11835617  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei.  
ORGANISM Trypanosoma brucei.  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
1 (bases 1 to 38)  
AUTHORS Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., McVernon, S.E., Razandreamanana, M.A., and Barrell, B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU92/4 GUTAT 10.1) was mechanically sheared to give a tight size distribution (~ 4 kb). The  $v + i$  method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsaved@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
Location/Qualifiers  
1. .38  
/organism="Trypanosoma brucei"  
/strain="TREU927"  
/db\_xref="taxon:5651"  
/clone="137c04"

FEATURES  
source  
1. .38  
/organism="Trypanosoma brucei"  
/strain="TREU927"  
/db\_xref="taxon:5651"  
/clone="137c04"  
BASE COUNT 9 a 11 c 14 g 4 t  
ORIGIN Query Match Best Local Similarity 50.4%; Score 11.6; DB 17; Length 38; Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CGGCTCGAGGGGG 22  
Db 18 CAGCHACGAGGGGTA 35

RESULT 11  
A2800550/c  
LOCUS A2800550 39 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0058E0R Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0215F10 R, DNA sequence.  
ACCESSION A2800550  
VERSION A2800550.1 GI:12952808  
KEYWORDS GSS.

SOURCE	house mouse.
ORGANISM	Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	Dunn, D., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhäusern, A. and Wright, D. Weiss, R.
AUTHORS	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center
FEATURES	High quality sequence stop: 39.
source	location/Qualifiers 1..39 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" (clone="UUGC2M058E10" /clone_libr="Mouse 10kb plasmid UGGC1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: pMD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource <a href="http://www.Jax.org/resources/documents/dnare/">http://www.Jax.org/resources/documents/dnare/</a> . The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1:4732114[gb] [REF29072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." Stratagene) cells
BASE COUNT	3 a 12 c 18 g 6 t
ORIGIN	50 4%; Score 11.6; DB 17; Length 39; Best Local Similarity 77.8%; Pred. No. 3.9e-05; Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	6 GGCTCGAGGGGGAAAC 23
Db	28 GGCCCCAGGGGGGAC 11
RESULT 12	36 bp mRNA linear EST 24-FEB-1996
LOCUS	AB25458
DEFINITION	o64f12..81 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1416431 3, 1996
VERSION	1 (bases 1 to 37)
KEYWORDS	similar to TR:000165 000165 HAX-1., mRNA sequence.
ACCESSION	AB25458
VERSION	AB25458.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	Dunn, D., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhäusern, A. and Wright, D. Weiss, R.
AUTHORS	Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: gappar-r@mail.nih.gov
FEATURES	High quality sequence stop: 1.
source	location/Qualifiers 1..36 /organism="Homo sapiens" /ab_xref="taxon:9606" /clone="IMAGE:116431" /clone_libr="NCI CGAP Lu5" /tissue_type="carcinoid" /lab_host="DH10B" /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT	4 a 8 c 9 g 15 t
ORIGIN	Query Match 49.6%; Score 11.4; DB 9; Length 36; Best Local Similarity 71.4%; Pred. No. 4.7e+05; Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	3 ATCCGGCTCGAGGGGGAAAC 23
Db	8 ATCTGCTTGTGTTGGTTAC 28
RESULT 13	37 bp mRNA linear EST 31-JUL-1995
LOCUS	H43693
DEFINITION	Y080b05..81 Soares adult brain N2b4H855Y Homo sapiens cDNA clone IMAGE:184209 3' Similar to SP:RS5_RAT P24050 40S RIBOSOMAL PROTEIN
VERSION	H43693
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	Hillier, L., Clark, N., Dubroque, T., Elliston, K., Hawkins, M., Holman, M., Holtzman, M., Kucaba, T., Le, M., Lennon, G., Marrs, M., Parsons, J., Riekin, D., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
AUTHORS	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson, R.K. Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)

Insert Size: 851

High quality sequence starts: 1

Source: IMAGE Consortium, LBL

This clone is available royalty-free through LBL ; contact the

IMAGE Consortium (<http://image.llnl.gov>) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert length: 851 Std Error: 0.00

Seq primer: Promega - 21ml3

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1. 37 /organism="Homo sapiens"

/db\_xref="GDB:3828558"

/db\_xref="taxon:9606"

/clone="IMAGE:184209"

/clone lib="Seares adult brain N2b4HB55Y"

/sex="Male"

/dev\_stage="55-year old"

/lab\_hos="DHIB (ampicillin resistant)"

/note="Organ: brain; Vector: pTR102 (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTCCAACTGAGGAGGGAGCCGCGCCCTTTTTTTTTTTTTTTT 3']

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pTR3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 53. Library constructed by Bento

Soares and M. Fatima Bonaldo. The adult brain RNA was

provided by Dr. Donald H. Gilden. Tissue was acquired

17-18 hours after death which occurred in consequence of a

ruptured aortic aneurysm. RNA was prepared from a pool of

tissues representing the following areas of the brain:

frontal, parietal, temporal and occipital cortex from the

left and right hemispheres, subcortical white matter, basal

ganglia, thalamus, cerebellum, midbrain, pons and

medulla." 6 a 8 c 11 g 10 t 2 others

BASE COUNT

ORIGIN

Query Match 49.6%; Score 11.4; DB 14; Length 37; Best Local Similarity 65.2%; Pred. No. 4.8e+05; Matches 15; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AAATGGCTCGAGCGGGAAAC 23 Db 32 ACACCTGCTNANAGCGGAGACC 10

RESULT 14

AU24523 AU254523 27 bp mRNA linear EST 25-APR-2002

LOCUS AU254523 3' -directed mouse cDNA library Mus musculus CDNA clone

DEFINITION BE0002375 3', mRNA sequence.

ACCESSION D18732

DEFINITION MUSQ50-794 Mouse 3'-directed Mus musculus domesticus cDNA clone

VERSION D18732.1

KEYWORDS EST.

SOURCE Mus musculus domesticus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 27)

AUTHORS Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.

TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed cDNA sequencing

COMMENT Unpublished (1995)

Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara

K.

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Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: [kikuya@nara.ac.jp](mailto:kikuya@nara.ac.jp)

URL: <http://love2.aist-nara.ac.jp/BED/index.html>

FEATURES

source

1. .27 /organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="BED002375"

/clone lib="3'-directed mouse cDNA library"

/tissue type="brain"

/note="vector: pGEM-T-easy"

/clone="3'-directed mouse cDNA library"

/note="vector: pGEM-T-easy"

/clone lib="3'-directed mouse cDNA library"

/note="vector: pGEM-T-easy"

Query Match 48.7%; Score 11.2; DB 9; Length 27; Best Local Similarity 81.2%; Pred. No. 5.6e+05; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

BASE COUNT

ORIGIN

7 a 5 c 9 g 6 t

FEATURES

source

1. .27 /organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="BED002375"

/clone lib="3'-directed mouse cDNA library"

/note="vector: pGEM-T-easy"

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BASE COUNT

ORIGIN

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/clone="BED002375"

/clone lib="3'-directed mouse cDNA library"

/note="vector: pGEM-T-easy"

/clone lib="3'-directed mouse cDNA library"

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